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A COCOA GENETIC LINKAGE MAP AND QTL DETECTION FOR WITCHES' BROOM RESISTANCE.

C.T. GUIMARAES¹, V.T. Queiroz¹, J.W.S. Mota¹, M.G. Pereira², R.F. Daher², V.R.M. Miranda², D. Anher³, E.G. Barros¹, M.A. Moreira¹

¹BIOAGRO - UFV, Vicosa, MG 36571-000, Brasil

²CCTA - UENF, Campos dos Goytacases, RJ 28015-260, Brasil

³CEPEC/CEPLAC, CP 7, Itabuna, BA 45600-000, Brasil

Witches' broom is a serious cocoa disease caused by the fungus *Crinipellis pernicioso*. This disease is one of the most limiting factor for the cocoa production in South America, Central America and Caribe. In Brazil, mainly in the state of Bahia, the witches' broom is spread over almost all cocoa farm causing serious economic, social and ecological damages. The aim of this work was to construct a cocoa genetic map and to use molecular markers to identify genomic regions associated with witches' broom resistance. We analysed 82 F2 individuals derived from a cross between Scavinia-6 (resistant) and ICS-1 (susceptible). The phenotypic evaluation for resistance, in numbers of brooms per cocoa tree, was performed at CEPEC/CEPLAC-Bahia. More than one hundred RAPD polymorphisms were scored in the parents and in the F2 progeny. The linkage map was constructed using MapMaker v3.0. Single and multiple regression models, interval mapping and composite interval mapping were used to map QTLs associated with witches' broom resistance. Significance threshold were determined by a thousand permutations in the phenotypic data. We found three markers significantly ($t\alpha.005$ and by permutation tests) associated with witches' broom resistance. QTL mapping identified the location and the effects of each marker. The genetic map will be used in marker assisted selection in cocoa breeding programs aiming to select for, among other traits, resistant genotypes. Financial Support: CNPq, CAPES and CEPEC/CEPLAC - Bahia.

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